

BLAST Basic Local Alignment Search Tool

Job Title: Nucleotide sequence (1935 letters)

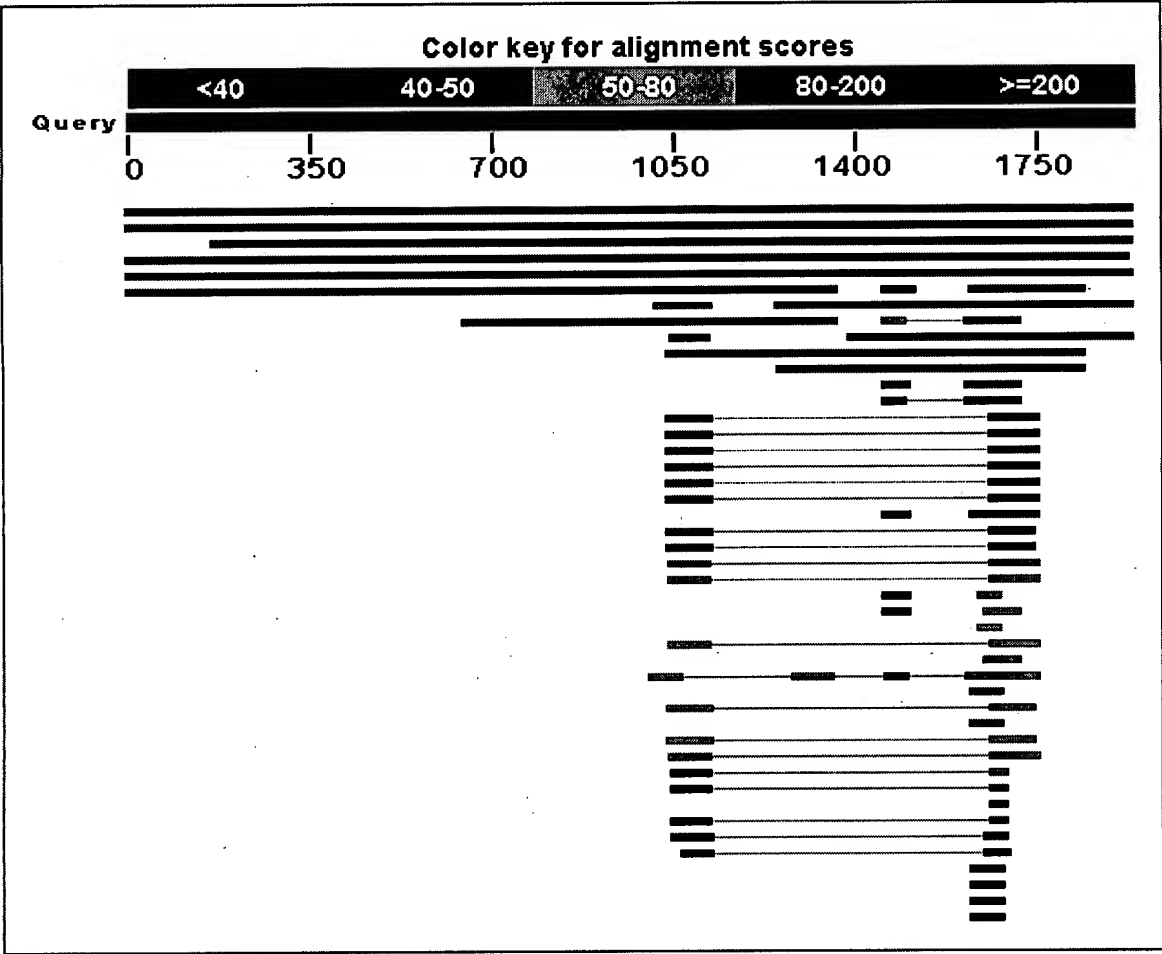
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•
•

BLASTN 2.2.17 (Aug-26-2007)

RID: HHG6MUYH01N Database: "Geo" 283,711 sequences; 1,244,709,904 total letters

Query= Length=1935

Distribution of 78 Blast Hits on the Query Sequence



Distance tree of results **NEW**

Sequences producing significant alignments:			Score (Bits)	E Value	
gi 34526552 dbj AK131104.1	Homo sapiens mRNA for FLJ00341 prote	3721	0.0	UEG	
gi 20521076 dbj AB011112.3	Homo sapiens mRNA for KIAA0540 prote	3715	0.0	UEG	
gi 38174270 gb BC060874.1	Homo sapiens neurobeachin-like 2, ...	3386	0.0	UEG	
gi 109483997 ref XM_236649.4	PREDICTED: Rattus norvegicus ne...	2267	0.0	UEG	
gi 51765227 ref XM_150243.4	PREDICTED: Mus musculus cDNA sequen	2040	0.0	E	
gi 27469592 gb BC042396.1	Mus musculus neurobeachin-like 2, ...	1413	0.0	UEG	
gi 23242934 gb BC035894.1	Homo sapiens neurobeachin-like 2, ...	1258	0.0	UEG	
gi 22902315 gb BC037746.1	Mus musculus neurobeachin-like 2, ...	873	0.0	UEG	
gi 30851326 gb BC052551.1	Mus musculus cDNA clone IMAGE:3469056	727	0.0	UE	
gi 37994643 gb BC060141.1	Mus musculus neurobeachin like 1, ...	212	3e-52	UEG	
gi 33417008 gb BC055813.1	Mus musculus neurobeachin like 1, ...	196	1e-47	UEG	
gi 26334212 dbj AK041108.1	Mus musculus adult male aorta and...	137	1e-29	UEG	
gi 39930598 ref NM_172882.2	Mus musculus WD repeat and FYVE ...	98.7	5e-18	UEG	
gi 26006236 dbj AB093277.1	Mus musculus mRNA for mKIAA0993 prot	98.7	5e-18	UEG	
gi 109499466 ref XM_223196.4	PREDICTED: Rattus norvegicus WD...	93.0	2e-16	UEG	
gi 117956398 ref NM_030695.2	Mus musculus LPS-responsive bei...	87.2	1e-14	UEG	
gi 26330689 dbj AK035483.1	Mus musculus adult male urinary b...	87.2	1e-14	UEG	
gi 26327124 dbj AK031216.1	Mus musculus 13 days embryo forel...	87.2	1e-14	UEG	
gi 10257400 gb AF188506.1 AF188506	Mus musculus LBA isoform beta	87.2	1e-14	UEG	
gi 10257404 gb AF188507.1 AF188507	Mus musculus LBA isoform gamm	87.2	1e-14	UEG	
gi 10180265 gb AF187731.1 AF187731	Mus musculus LBA (Lba) mRNA,	87.2	1e-14	UEG	
gi 10439364 dbj AK026491.1	Homo sapiens cDNA: FLJ22838 fis, ...	85.3	5e-14	E	
gi 109466822 ref XM_001066755.1	PREDICTED: Rattus norvegicus...	81.4	7e-13		
gi 109465018 ref XM_342271.3	PREDICTED: Rattus norvegicus LP...	81.4	7e-13		
gi 26335530 dbj AK043125.1	Mus musculus 7 days neonate cereb...	62.2	5e-07	EG	
gi 11863683 emb Y18276.1 MMU18276	Mus musculus mRNA for neurobea	62.2	5e-07	UEG	
gi 1556398 emb X96586.1 HSFAN	H.sapiens mRNA for FAN protein	62.2	5e-07	UEG	
gi 10440523 dbj AK024502.1	Homo sapiens mRNA for FLJ00111 prote	62.2	5e-07	UEG	
gi 31543296 ref NM_003580.2	Homo sapiens neutral sphingomyel...	62.2	5e-07	UEG	
gi 5305402 gb AF072372.1 AF072372	Mus musculus lysosomal traf...	62.2	5e-07	UEG	
gi 10047288 dbj AB046827.1	Homo sapiens mRNA for KIAA1607 prote	62.2	5e-07	UEG	
gi 113194865 gb AE014296.4	Drosophila melanogaster chromosome 3	58.4	6e-06	E	
gi 113193577 gb AE014298.4	Drosophila melanogaster chromosome X	58.4	6e-06	E	
gi 16716612 gb AF216648.2 AF216648	Homo sapiens LPS responsiv...	58.4	6e-06	UEG	
gi 15291502 gb AY051596.1	Drosophila melanogaster GH23814 full	58.4	6e-06	UE	
gi 1580780 gb M83822.1 HUMCDC4REL	Human beige-like protein (BGL)	58.4	6e-06	UEG	
gi 113194944 gb AE014134.5	Drosophila melanogaster chromosome 2	56.4	2e-05	E	
gi 109466684 ref XM_001059612.1	PREDICTED: Rattus norvegicus...	56.4	2e-05	EG	
gi 62422576 ref NM_015678.3	Homo sapiens neurobeachin (NBEA), m	52.6	4e-04	UEG	
gi 21434742 gb AF467288.1	Homo sapiens BCL8B protein (BCL8B) mR	52.6	4e-04	UEG	
gi 6808382 emb AL137748.1 HSM802363	Homo sapiens mRNA; cDNA D...	52.6	4e-04	UEG	
gi 10047152 dbj AB046764.1	Homo sapiens mRNA for KIAA1544 prote	52.6	4e-04	UEG	
gi 42566099 ref NM_115956.2	Arabidopsis thaliana beige/BEACH...	48.8	0.005	UEG	
gi 74199109 dbj AK155186.1	Mus musculus NOD-derived CD11c +v...	46.8	0.019	UEG	
gi 16758279 ref NM_053518.1	Rattus norvegicus lysosomal traf...	46.8	0.019	UEG	
gi 111955375 ref NM_010748.2	Mus musculus lysosomal trafficking	43.0	0.28	UEG	
gi 109503753 ref XM_001060720.1	PREDICTED: Rattus norvegicus...	43.0	0.28	EG	

<u>gi 26342211 dbj AK051786.1 </u>	Mus musculus 12 days embryo spina...	<u>43.0</u>	0.28	EG
<u>gi 1813541 gb U70015.1 MMU70015</u>	Mus musculus lysosomal traffi...	<u>43.0</u>	0.28	UEG
<u>gi 1675213 gb U52461.1 MMU52461</u>	Mus musculus beige (bg) mRNA, pa	<u>43.0</u>	0.28	UEG
<u>gi 31317271 ref NM_014991.3 </u>	Homo sapiens WD repeat and FYVE ...	<u>41.1</u>	1.0	UEG
<u>gi 23194376 gb AF538685.1 </u>	Homo sapiens ALFY mRNA, complete cds	<u>41.1</u>	1.0	EG
<u>gi 34367312 emb BX648153.1 HSM808300</u>	Homo sapiens mRNA; cDNA DKF	<u>41.1</u>	1.0	UEG
<u>gi 20521719 dbj AB023210.2 </u>	Homo sapiens mRNA for KIAA0993 prote	<u>41.1</u>	1.0	UEG

Database: "Geo"

Posted date: Sep 26, 2007 5:53 PM

Number of letters in database: 1,268,626,203

Number of sequences in database: 291,671

Lambda K H
1.33 0.621 1.12

Gapped
Lambda K H
1.33 0.621 1.12

Matrix: blastn matrix:1 -2

Gap Penalties: Existence: 5, Extension: 2

Number of Sequences: 291671

Number of Hits to DB: 190948

Number of extensions: 15

Number of successful extensions: 13

Number of sequences better than 10: 8

Number of HSP's better than 10 without gapping: 0

Number of HSP's gapped: 13

Number of HSP's successfully gapped: 10

Length of query: 1935

Length of database: 1268626203

Length adjustment: 24

Effective length of query: 1911

Effective length of database: 1261626099

Effective search space: 2410967475189

Effective search space used: 2410967475189

A: 40

X1: 11 (21.1 bits)

X2: 31 (59.6 bits)

X3: 52 (100.0 bits)

S1: 15 (29.5 bits)

S2: 20 (39.1 bits)



UniGene

ORGANIZED VIEW OF THE TRANSCRIPTOME

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UGID:232080 UniGene Hs.437043 *Homo sapiens* NBEAL2

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Neurobeachin-like 2 (NBEAL2)

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SELECTED PROTEIN SIMILARITIES

Comparison of sequences in UniGene with selected protein reference sequences. The alignments can suggest function of a gene.

	Reference Protein	Species	Id(%)	Len(aa)
NP_055990.1	neurobeachin-like 2	<i>H. sapiens</i>	100.0	2753
XP_236649.4	PREDICTED: similar to neurobeachin-like 1	<i>R. norvegicus</i>	91.9	2744
XP_982666.1	PREDICTED: neurobeachin-like 2	<i>M. musculus</i>	90.8	2749
XP_690862.1	PREDICTED: similar to neurobeachin-like 1	<i>D. rerio</i>	74.3	842
NP_647876.1	CG1332-PA	<i>D. melanogaster</i>	58.6	868
XP_421964.1	PREDICTED: similar to FLJ00341 protein	<i>G. gallus</i>	57.1	2690
NP_009961.2	beige protein homologue 1; Bph1p	<i>S. cerevisiae</i>	55.1	394
XP_324851.1	hypothetical protein	<i>N. crassa</i>	48.3	547
NP_564728.2	unknown protein	<i>A. thaliana</i>	47.5	736
NP_502422.1	VT23B5.2	<i>C. elegans</i>	47.1	537
NP_001018801.1	hypothetical protein SPBC3H7.16	<i>S. pombe</i>	45.7	576

GENE EXPRESSION

Tissues and development stages from this gene's sequences survey gene expression. Links to other NCBI expression resources.

[Expression Profile: View expression levels using UniGene's EST ProfileViewer](#)

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Note: Highly represented (1.0 pct) in cDNA library dbEST:7892, EN0065.

GEO profiles: Gene expression profiles in the NCBI Gene Expression Omnibus database

MAPPING POSITION

Genomic location specified by transcript mapping, radiation hybrid mapping, genetic mapping or cytogenetic mapping.

Chromosome:

3

Map position:

3p21.31

SEQUENCES

Sequences representing this gene; mRNAs, ESTs, and gene predictions supported by transcribed

sequences.

mRNA sequences (9)

AK131104.1	Homo sapiens mRNA for FLJ00341 protein	P
AY358455.1	Homo sapiens clone DNA35680 SQFE253 (UNQ253) mRNA, complete cds	P
BC060874.1	Homo sapiens neurobeachin-like 2, mRNA (cDNA clone IMAGE:30348606), partial cds	PA
NM_015175.1	Homo sapiens neurobeachin-like 2 (NBEAL2), mRNA	PA
AK074036.1	Homo sapiens mRNA for FLJ00082 protein	P
AK092871.1	Homo sapiens cDNA FLJ35552 fis, clone SPLEN2004346	P
BC029944.1	Homo sapiens neurobeachin-like 2, mRNA (cDNA clone IMAGE:5189816)	P
BC035894.1	Homo sapiens neurobeachin-like 2, mRNA (cDNA clone IMAGE:5219805), with apparent retained intron	P
AB011112.3	Homo sapiens mRNA for KIAA0540 protein, partial cds	P

EST sequences (10 of 384) [Show all sequences]

AA926792.1	Clone IMAGE:1552328	3' read
AA927544.1	Clone IMAGE:1552618	3' read P
A146791.1	Clone IMAGE:1706723	3' read P
CB049571.1	Clone IMAGE:3271458	3' read P
CB049572.1	Clone IMAGE:3271458	5' read P
CB051391.1	Clone IMAGE:3289353	5' read P
A147562.1	Clone IMAGE:1555699	3' read P
CB070301.1	Clone IMAGE:6554218	3' read
CB070359.1	Clone IMAGE:6554218	5' read P
A1202100.1	Clone IMAGE:1860078	3' read

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Key to Symbols

P Has similarity to known **Pro**teins (after translation)
A Contains a poly-**A**denylation signal
S Sequence is a **S**uboptimal member of this cluster
M Clone is putatively CDS-complete by **MGC** criteria



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Range: from to Features: ☒ CDD

☐ 1: [NP_055990](#). Reports neurobeachin-like...[gi:149944548]

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LOCUS NP_055990 2754 aa linear PRI 29-JUN-2007
DEFINITION neurobeachin-like 2 [Homo sapiens].
ACCESSION NP_055990 XP_291064 XP_946304
VERSION NP_055990.1 GI:149944548
DBSOURCE REFSEQ: accession [NM_015175.1](#)
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM [Homo sapiens](#)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 Catarrhini; Hominidae; Homo.
REFERENCE 1 (residues 1 to 2754)
AUTHORS Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,
 Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,
 Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E.,
 Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S.,
 Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C.,
 Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V.,
 Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Wieand,D., Woods,K.,
 Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,
 Goddard,A., Wood,W.I., Godowski,P. and Gray,A.
TITLE The secreted protein discovery initiative (SPDI), a large-scale
 effort to identify novel human secreted and transmembrane proteins:
 a bioinformatics assessment
JOURNAL Genome Res. 13 (10), 2265-2270 (2003)
PUBMED [12975309](#)
REMARK Erratum:[Genome Res. 2003 Dec;13(12):2759]
COMMENT **VALIDATED REFSEQ:** This record has undergone preliminary review of
 the sequence, but has not yet been subject to final review. The
 reference sequence was derived from [CR988681.1](#), [AK131104.1](#),
 [AB011112.3](#) and [BC060874.1](#).
 On or before Jun 29, 2007 this sequence version replaced
 gi:[113414493](#), gi:[113415050](#).
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 /map="3p21.31"
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 Region 1918..2003
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 protein Nerubeachin, N-terminal to the BEACH domain;
 cd01201"
 /db_xref="CDD:29850"

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 /note="Beige/BEACH domain; pfam02138"
 /db_xref="CDD:65883"
Region 2464..2713
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 /note="WD40 domain, found in a number of eukaryotic
 proteins that cover a wide variety of functions including
 adaptor/regulatory modules in signal transduction,
 pre-mRNA processing and cytoskeleton assembly; typically
 contains a GH dipeptide 11-24 residues from; cd00200"
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Site order(2476,2481,2487..2488,2500..2501,2519,2523,
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ORIGIN

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2701 hvlvgledgk livvvagqps evrssqfark lwrssrrisq vssgeteynp tear

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Aug 28 2007 16:53:42